

The present invention relates to adjuvants which are intended to be attached to a molecule in order to improve its activity, in particular to increase the strength of the immune response. It also relates to
5 complexes which contain such an adjuvant attached to an active molecule.

The active molecule can, in particular, be a protein, a peptide, a polysaccharide, an oligosaccharide or a DNA or RNA nucleic acid.

10 The development of vaccines which are perfectly defined and which lack pronounced side effects requires the use of immunizing antigens of low molecular weight such as peptides or oligosaccharides. These antigens of low molecular weight, and also certain antigens of higher
15 molecular weight, such as bacterial wall polysaccharides, cannot, on their own, induce a lasting, powerful immune response. It is essential to link these antigens to carrier proteins by chemical means or by using genetic manipulation.

20 The carrier proteins which are currently employed are of two types:

- tetanus and diphtheria toxoids: too frequent use of these carrier proteins risks jeopardizing a strong response to the hapten and risks the possibility of
25 problems with immunotoxicity,
- a membrane protein extract from *Neisseria meningitidis* (OMPC): consists of a membrane protein which is contaminated with lipids and LPS.

30 Patent EP-267 204 proposed using a support molecule which is intended to be coupled to an immunogen and which consists of an *E. coli* or *salmonella* membrane protein.

35 The Applicant has demonstrated that a protein which is extracted from the outer membrane of *Klebsiella pneumoniae* considerably improves the immune response to an antigen or a hapten when it is administered to a host at the same time as the latter. More particularly, an OmpA protein, the P40 protein of *K. pneumoniae*, can be used as an adjuvant in immunogenic complexes when it is

attached to an immunogenic element.

The chemical conjugates which are derived by coupling peptides to the P40 give good results, and an assessment of the immune response shows antibody
5 responses to these peptides which are greater than those which are observed when KLH or TT reference carrier proteins are used.

However, the peptide antigens are preferentially attached to the C-terminal part of the sequence, which is
10 the most immunogenic part of the molecule (Puohiniemi, R et al., 1990, Infect Immun. 58, 1691-1696). This can present a serious problem in the case of fusion proteins which contain the complete P40 sequence. Therefore, use of a fragment of the sequence which supports the adjuvant
15 activity would have a greater effect in minimizing the immunogenicity of the carrier protein and the risks associated with this immunogenicity.

For this reason, the present invention relates to an immunogenic complex of the type which comprises an
20 immunogenic element which is attached to an adjuvant which increases the strength of the immune response, characterized in that the immunogenic element is an antigen or a hapten, and in that the adjuvant comprises at least a part of the P40 protein of *Klebsiella pneumoniae* or a protein which exhibits at least 80%
25 homology, and preferably at least 90% homology, with the P40 protein.

In particular, the invention relates to an adjuvant which consists of a protein or a peptide having
30 the P40 sequence which is substantially devoid of the immunogenic parts.

These P40 fragments according to the invention are, in particular:

- the P40 sequence which lacks the immunogenic peri-plasmic C-terminal part,
35
- a sequence which contains the third and the fourth extramembrane loops flanking an intramembrane sequence,
- a sequence which contains one invariant

extramembrane loop and the adjacent intramembrane sequence.

Those P40 sequences are defined as invariant extramembrane loops which are homologous with the sequences of the loops which are conserved between different enterobacterial species. The sequences of the extramembrane loops which are not conserved during the course of evolution are termed variable loops. The extramembrane loops are located in accordance with the Vogel and Jahnig model (1986, J. Mol. Biol., 190: 191-199), which relates to E. coli OmpA.

The choice of the fragments and, more particularly, the third sequence (amino acids 127 to 179) is based on the hypothesis according to which the invariant extramembrane loops (conserved between the OmpAs of the different enterobacteria) contain sequences which are recognized by immunocompetent cells, with these latter being able to have receptors which recognize these sequences.

The specific recognition of these sequences by antigen-presenting cells would make it possible to target antigens towards these cells and thus to induce an adjuvant effect.

For this reason, the invention also relates to an adjuvant product which consists of the sequence encompassed between amino acids 1 to 179 of the P40 protein of K. pneumoniae, or to a sequence which exhibits at least 80%, and preferably at least 90%, homology with the sequence which is encompassed between amino acids Nos. 1 and 179 of the sequence of the P40 protein of K. pneumoniae.

The invention furthermore relates to an adjuvant which consists of the sequence which is encompassed between amino acids 108 to 179 of the P40 protein of K. pneumoniae, or to a sequence which exhibits at least 80% homology, and preferably at least 90% homology, with the sequence which is encompassed between amino acids nos. 108 and 179 of the P40 protein of K. pneumoniae.

According to another aspect, the invention

relates to an adjuvant which consists of the sequence which is encompassed between amino acids nos. 127 to 179 of the P40 protein of *K. pneumoniae*, or to a sequence which exhibits at least 80%, and preferably at least 90%,
5 homology with the sequence which is encompassed between amino acids nos. 127 to 179 of the P40 protein of *K. pneumoniae*.

The sequences ID No. 2, ID No. 4, ID No. 6 and ID No. 8 correspond to adjuvants according to the invention.
10 This protein, and these peptide adjuvants, can, in particular, be prepared from membranes of bacteria of the species *Klebsiella pneumoniae*. The process then comprises the following steps:

- 15 a) precipitating the lipopolysaccharides by adding detergent and a salt of a divalent cation, and recovering the supernatant,
- b) precipitating the proteins from the supernatant and resuspending the sediment,
- 20 c) chromatographing the suspension on an anion exchanger and recovering the fractions which contain the adjuvant product,
- d) chromatographing on a cation exchanger and recovering the fraction which contains the adjuvant product,
- 25 e) concentrating the fraction obtained from step d) in order to recover an adjuvant product in the form of protein or peptide which is essentially free of liposaccharides.

Dialysis steps can advantageously be interposed
30 between steps b) and c), and steps c) and d), respectively.

The invention also relates to immunogenic complexes which can be obtained using the different adjuvants.

35 The adjuvant can be attached to the immunogenic element by chemical coupling.

This covalent coupling of the peptide hapten to the adjuvant can be effected in a manner which is well known in the state of the art. Reagents which are

appropriate for this purpose comprise, in particular, N-succinimide esters, carbodiimides, EEDQ (N-ethoxycarbonyl-2-ethoxy-1,2-dihydroquinoline) and the like.

5 The fragment of the P40 protein concerned, and the immunogenic element, can also be fused by means of genetic manipulation.

10 The fusion protein which is obtained between the fragment of the 40 protein and the immunogenic element can also be fused, by genetic manipulation, to a protein which is a receptor for a serum protein, in particular for human serum albumin.

15 The immunogenic element, an antigen or hapten, can, in particular, originate from viruses; those which may be mentioned are RSV (Respiratory Syncytial Virus) proteins or their fragments, for example protein G of RSV, or the hepatitis B antigen.

In the case of the RSV G protein, use may be made of the entire protein or of its fragments, where appropriate modified by point mutation or deletion.

20 The Applicant demonstrated that administration of a hapten coupled to a fragment of the P40 protein according to the invention resulted in a substantial increase in the immune response while limiting the risks of reactions against the adjuvant itself.

25 A process for increasing the immunogenicity of an antigen or of a hapten, characterized in that the said antigen or hapten is attached to an adjuvant which comprises all or part of the sequence of the P40 protein of *Klebsiella pneumoniae*, in the form of a complex as previously defined, is also part of the invention.

30 The invention also relates, therefore, to a vaccine, characterized in that it contains an immunogenic element attached to a fragment of the P40 protein which lacks a substantial part of the C-terminal sequence of the native P40 protein.

35 It also comprises pharmaceutical compositions which contain a complex which is formed between an adjuvant and an immunogenic element, as previously defined, and pharmaceutically acceptable excipients which

are suited to administration of the complex by the parenteral and/or oral routes.

The invention also relates to the nucleotide sequences which encode the previously described peptides or proteins, and to the use of these sequences as a medicament. More particularly, such DNA sequences can be used in compositions which are intended for immunization by the intramuscular or intradermal route.

The examples which follow are intended to illustrate the invention without limiting its scope in any way.

In these examples, reference will be made to the following figures:

Figure 1: Strategy for cloning P40 by gene amplification.

Figure 2: Cloning P40 into pVABBG2AC.

Figure 3: Choice of the different P40 fragments.

Figure 4: Cloning Δ P40G2AC into pVABB

Figure 5: Anti-G1AC peptide antibody response following immunizations with different concentrations of P40ext-G1AC.

Figure 6: Anti-G1AC peptide antibody response obtained using different immunization protocols.

Example 1: Isolation and purification of the p40 protein

Material and methods

Klebsiella pneumoniae (strain I-145, 40 g of dry cells) biomass is adjusted to pH 2.5 with pure acetic acid.

After having added a 1/2 volume of a solution containing 6% cetrимide, 60% ethanol and 1.5 M CaCl₂, the pH of which is adjusted to 2.5 with acetic acid, the mixture is left to stir at room temperature for 16 hours.

After the mixture has been centrifuged at 15,000 g for 20 min and at 4°C, the proteins in the supernatant are precipitated with ethanol. Two conse-

cutive precipitations, of 20 to 50% and then of 50 to 80%, are carried out with an intermediate centrifugation (10 min, 10,000 g, 4°C).

5 The pellets obtained after the second precipitation are resuspended in a 1% solution of zwittergent 3-14.

After the mixture has been stirred at room temperature for 4 hours, its pH is adjusted to 6.5 using 1N NaOH.

10 Centrifugation of the mixture at 10,000 g for 20 min and at 4°C yields a fraction which is enriched in membrane proteins (MP fraction).

15 The proteins of the MP fraction are dialysed against a 20 mM Tris/HCl, pH 8.0; 0.1% zwittergent 3-14 buffer. The dialysate is loaded onto a column containing a support of the strong anion exchanger type (column of $\varnothing = 50$ mm \times H = 250 mm, Biorad Macrorep High Q gel) which is equilibrated in the above-described buffer. The P40 protein is eluted at an NaCl concentration of 50 mM
20 in the equilibration buffer.

The fractions containing the P40 are pooled and dialysed against a 20 mM citrate, pH 3.0; 0.1% zwittergent 3-14 buffer. The dialysate is loaded onto a column containing a support of the strong cation exchanger type
25 (dimensions of the column: $\varnothing = 25$ mm \times H = 160 mm, Biorad Macrorep High S gel) which is equilibrated in the 20 mM citrate, pH 3.0; 0.1% zwittergent 3-14 buffer. The P40 protein is eluted at an NaCl concentration of 0.7 M. The fractions containing the P40 are pooled and concentrated
30 by ultrafiltration using a Minitan Millipore tangential flow filtration system employing membrane discs having a cutoff threshold of 10 kDa.

Results

35 The fractions obtained after each chromatographic step are analysed by SDS-PAGE in order to pool those which contain the P40 protein.

The protein quantities are measured by the Lowry

method (Table 1).

Table 1: Table summarizing the quantities of protein and LPS in the fractions obtained in the different steps of the process for purifying the P40 protein (n.d. = not determined)

	Proteins	Yield	LPS
Biomass	40 g	-	n.d.
MP fraction	900 mg	2.25%	n.d.
P40-enriched fraction	400 mg	1%	10%
P40 protein	130 mg	0.3%	< 1%

The purity and homogeneity of the P40 protein are assessed by SDS-PAGE.

After the cation exchange chromatography step, the P40 protein is free of the main contaminant present in the MP fraction (the protein has an apparent molecular weight of 18 kDa) and is more than 95% pure. Moreover, this purification step eliminates the lipopolysaccharides. This purification step was not present in the purification process which was previously presented.

The electrophoretic profile of the P40 gives several bands. These bands are revealed after immunoblotting with mouse anti-P40 monoclonal antibodies. The upper major band corresponds to the denatured protein (by treatment at 100°C for 15 min in the presence of SDS) and the lower minor band corresponds to the protein in its native form.

P40 is, therefore, a so-called heat-modifiable protein, and this property was checked by means of carrying out heating kinetics at 100°C in the presence of SDS. Without heating, the protein in its native form has a β -sheet structure which fixes more SDS and which therefore migrates further towards the anode than does the denatured form (complete denaturation after 5 min at 100°C), which exhibits an α -helical structure

(Keller, K.B. 1978 J. Bacteriol., 134, 1181-1183).

Contamination with lipopolysaccharides (LPS) is assessed by gas-phase chromatographic measurement of β -hydroxymyristic acid, which is a marker fatty acid for *Klebsiella pneumoniae* LPS (Table 1).

This method can only be used to approximate the content of LPS in the samples derived from the different purification steps.

Since the quantity of β -hydroxymyristic acid which was present in the P40 fraction after cation exchange chromatography was less than the measurement threshold, the quantity of residual LPS may be estimated to be less than 1%.

Example 2: Cloning and expressing the P40 protein

72% of the sequence of the OmpA gene of *Klebsiella pneumoniae* has been published by LAWRENCE et al., 1991, J. Gen. Microbiol., 137: 1911-1921).

The originality of our studies resides in determining all of the sequence, that is to say that corresponding to the 83 N-terminal amino acids and the 11 C-terminal amino acids (out of a total of 335 amino acids).

Material and method

Bacterial strains

E. coli: RV 308: strain ATCC 31608 (Maurer, R. et al., 1980, J. Mol. Biol., 139, 147-161).

K. pneumoniae: IP 145: strain C.I.B.P.F. - patent filed on 19 January 1981.

Vectors

* pRIT 28 (Hultman T. et al., 1988, Nucléosides Nucléotides, 7: 629-638): cloning and sequencing vector which possesses the gene for resistance to ampicillin, the origins of replication of E. coli and phage F1 and a portion of the E. coli (β -galactosidase) lac Z gene.

* pVABB: Gene fusion expression vector.

Solutions

- Gene amplification

Lysis buffer:

25 mM Taps,	pH 9.3
2 mM MgCl ₂ ,	

Amplification
buffer: 25 mM Tris, pH 9.3
2 mM MgCl₂
0.1% Tween 20
200 mM dNTP.

Purification of the proteins

20	TST (20x):	Tris base	0.5 M
		HCl	0.3 M
		NaCl	4 M
		Tween 20	1%
		EDTA	20 mM

Washing buffer:	Tris HCl	50 mM	pH 8.5
	MgCl ₂	5 mM	

25	Denaturation	Gua-HCl	7.8 M	
	solution:	Tris-HCl	28 mM	pH 8.5

Renaturation	Gua-HCl	0.5 M	
solution:	Tris-HCl	25 mM	pH 8.5
	NaCl	150 mM	
	Tween 20	0.05%	

5 Synthesis of the oligonucleotides

The choice of nucleotide primers was decided on the basis of the published part of the *Klebsiella pneumoniae* OMPA sequence (Lawrence, J.G. et al., 1991, J. Gen. Microbiol., 137: 1911-1921), the consensus
10 sequence derived from aligning the sequences of 5 enterobacteria (*E. coli*, *S. typhimurium*, *S. marcescens*, *S. dysenteriae* and *E. aerogenosae*) OMPAs, and peptide sequences which are obtained by manually sequencing.

The oligonucleotides were synthesized by the
15 phosphoramidite chemical method on a "Gene Assembler Plus" appliance from Pharmacia.

PCR gene amplification of the P40 gene

The DNA of the *Klebsiella pneumoniae* OMPA was amplified in the following manner.

20 A *Klebsiella pneumoniae* colony is lysed in 10 μ l of lysis buffer by being heated at 95°C for 5 minutes.

1 μ l of this solution serves as the DNA source for the amplification reactions.

These reactions are carried out in 100 μ l of
25 amplification buffer using 5 pmol of each primer and 1 unit of Taq polymerase enzyme (Perkin Elmer Cetus). Each cycle comprises one denaturation step of 30 seconds at 95°C, followed by hybridization of the primer to the DNA and an extension of one minute at 72°C. 30 cycles are
30 performed in this way using a Perkin Elmer Cetus "Gen Amp PCR" 9000 thermocycler.

The subsequent PCRs are carried out using previously amplified DNA fragments.

The amplified DNA fragments are then digested and
35 ligated to the pRIT 28 vector.

Sequencing

The fragments which have thus been cloned are sequenced on an Applied Biosystems 373 automated DNA Sequencer. The sequencing reactions are carried out using
5 the "Dye Terminator" kit in accordance with the supplier's (Applied Biosystems) recommendations either on double-stranded DNA obtained after gene amplification or derived from a maxiprep, or on single-stranded DNA derived from denatured PCR fragments (Hultman, T. et al.,
10 1989, Nucleic Acids Rev. 17: 4937-4946).

Expression of the protein

The entire P40 gene is cloned into the expression vector pVABB. This vector renders it possible to affix a "BB" affinity tail to P40, with B being the part of the
15 streptococcal G protein which binds serum albumin (Nygren, P.A. et al., 1988, J. Mol. Recognit. 1, 69-74).

The E. coli RV308 strains which have been transformed with the pVABBP40 vector are cultured, at 37°C, overnight and with stirring, in 100 ml of TSB which is
20 supplemented with yeast extract, ampicillin (200 µg/ml), tetracycline (8 µg/ml) and tryptophan (100 µg/ml). On the following day, a culture of OD = 1 at 580 nm wavelength is prepared in TSB + yeast extracts + amp + tet.

After culturing for 10 minutes, expression of the
25 protein is induced by adding IAA (25 µg/ml) to the medium. The culture is centrifuged at 2460 g for 10 minutes at 4°C.

The pellet is taken up in 20 ml of 1 × TST, pH 7.4, and the solution is then centrifuged at 23,000 g
30 for 30 minutes at 4°C.

The supernatant is passed through HSA Sepharose, enabling the so-called soluble proteins to be isolated. The pellet is washed with washing buffer and then centrifuged at 23,000 g for 30 minutes at 4°C. The pellet
35 containing the inclusion bodies is then taken up in 900 µl of a denaturing solution + 100 µl of 10 mM dithio-

threitol and this solution is incubated at 37°C for 2 hours.

The solution is then incubated, at room temperature, overnight and with stirring, in 100 ml of renaturation buffer and then centrifuged at 23,000 g for 30 minutes at 4°C.

The supernatant is passed through HSA Sepharose.

In the two cases, the bound proteins are eluted with 0.5 M acetic acid, pH 2.8, and collected in 1 ml fractions.

The collected fractions are then analysed by SDS-PAGE gel electrophoresis and immunoblotting.

Results

The gene was cloned in three stages in accordance with the strategy depicted in Figure 1.

In a first stage, we confirmed the published part of the sequence with the exception of a T in place of an A in position 103.

We then determined the 3' sequence of the gene and, after that, the 5' sequence.

The entire gene was obtained by fusing the two parts 8/4 and 3/14 and then cloned into the pRIT 28 vector. The sequence is sequence ID No. 1.

The protein is expressed in the BBP40 form.

It is mainly obtained from inclusion bodies. Some fifty milligrams of protein are purified from a 200 ml culture.

The electrophoretic profile demonstrates that BBP40, which is obtained after denaturation, is of high purity. The apparent molecular weight corresponds to the calculated theoretical weight, which is 63 kDa.

Immunoblot characterization demonstrates that the purified protein is well recognized by a rabbit anti-P40 serum.

Example 3: BBP40G2ΔC fusion protein, subgroup a

An oligonucleotide was synthesized which corresponded to the N-terminal part of the gene from which the stop codon had been deleted.

5 The 5' part was amplified by PCR, purified, cloned into the pRIT 28 vector, and sequenced by the method described in Example 2.

In a second stage, the two parts of the gene were fused and cloned into vector pVABBG2ΔC (Figure 2). G2ΔC
10 represents the sequence of a 101 amino acid fragment of the G protein of respiratory syncytial virus G (130-230).

E. coli bacteria of the RV308 strain are then transformed with the pVABBG2ΔC vector.

15 The proteins which are produced are purified as already described for BBP40.

Results

The BBP40G2ΔC protein is mainly obtained from the inclusion bodies. Some twelve mg of proteins are purified from 200 ml of culture medium.

20 The protein is fairly pure by electro-phoresis.

The apparent molecular weight corresponds to the calculated theoretical weight, which is 75 kDa.

Example 4: Cloning and expressing three P40 fragments

Material and methods

25 The oligonucleotides

Three oligonucleotides were synthesized which were complementary to the P40 sequence: 16-17-18 (cf. Figure 3).

30 Defined parts of the gene were then amplified by PCR using the DNA from a miniprep (Applied protocol) of pRIT 28 P40.

In this way, it was possible to clone the part of

the gene corresponding to all the transmembrane part
(8/17, termed fragment No. 8) to two external loops and
two transmembrane portions (16/17, termed fragment
No. 16), and to 1 external loop and two transmembrane
5 portions (18/17, termed fragment No. 18).

The DNA fragments which have thus been amplified
are digested and then isolated and ligated into the
pRIT 28 vector and sequenced (cf. BBP40 cloning of P40).

The BBAP40G2ΔC fusion protein

10 The G2ΔC gene is isolated by digesting the vector
pRIT 28 G2ΔC and then ligated into the digested vector
pRIT 28 ΔP40 (ΔP40 represents one of the P40 fragments).

Subsequently, the entire ΔP40G2ΔC is isolated by
digestion and cloned into pVABB (cf. Figure 4).

15 The three hybrid proteins are expressed in
accordance with the protocol described for BBP40.

Results

Just like BBP40 and BBP40G2ΔC, BB8G2ΔC is mainly
obtained from the inclusion bodies. A 400 ml culture
20 yields some ten mg of protein.

By contrast, most of the proteins BB18G2ΔC and
BB16G2ΔC are present in the soluble form at the sonica-
tion step. In each case, some ten mg are obtained per
400 ml of culture.

25 These proteins were characterized by SDS-PAGE-
electrophoresis. Their molecular weight corresponds to
the calculated theoretical weight:

	BB8G2ΔC	58.03 kDa
	BB16G2ΔC	46.5 kDa
30	BB18G2ΔC	45.5 kDa

In a Western blot, the three hybrids are recog-
nized just as well by an anti-G2 polyclonal antibody as
by anti-P40 antibody.

Example 5

1. Effects of the P40 protein on cells of the immune system

1.a. B lymphocytes

5 30 μ g of P40, obtained by extracting the membrane (P40 ext) or by genetic recombination (rec P40, i.e. BBP40), were injected subcutaneously into BALB/c mice (5 per group) on days 0 and 21. The immunizations were carried out without using any adjuvant. 10 days after the
10 last immunization, the anti-P40ext antibody response was assessed in individual sera by the ELISA method. Table 2 gives the mean of the titres obtained on 5 samples. The negative controls did not contain any anti-P40ext antibody.

15 Table 2: Anti-P40ext antibody response

Immunizations with:	xtP40	recP40
Antibody titres:	87040	112640

Under these experimental conditions, the P40rec is as immunogenic as the P40ext. These two proteins
20 therefore contain B epitopes which interact with the B lymphocytes.

1.b. T lymphocytes

The delayed hypersensitivity reaction (HSR) to P40ext was measured by the deferred paw-pad swelling
25 test. BALB/c mice (5 per group) were sensitized subcutaneously with 100 μ g of P40ext without any adjuvant. After 6 to 10 days, the mice were stimulated subcutaneously with 100 μ g of P40ext/20 μ l in the right posterior paw pad while the left posterior paw pad was

given PBS. The swelling of the paw pad was measured 24 hours later. No delayed hypersensitivity is observed in the negative control (5 non-sensitized mice).

5 Table 3: Delayed hypersensitivity reaction induced by P40ext, measured by swelling of the paw pad (in mm)

D6		D10	
BALB/c	C57B1/6	BALB/c	C57B1/6
7.9	7.8	7.5	7.4

10 The results shown in Table 3 indicate that the mice immunized with P40ext produce highly quantitative delayed hypersensitivity reactions in the paw pad. The HSR reaction reflects the cell-mediated immune response, which requires Th1 cells. From this, it may be concluded that P40ext contains at least one T epitope which is able to promote the Th1 response, without MHC restriction.

15 1.3 Macrophages

20 The effect of P40ext on macrophages was determined by their production of nitrite. RAW 264.7 cells, which are mouse monocyte-macrophages, were incubated, at 37°C for 72 hours, in the presence of different concentrations of P40ext. The quantities of nitrites in the supernatants of the cell-cultures were measured by colorimetry using the Griess-Ilosvay reagent.

25 The production of nitrite reflects activation of the macrophages and plays a crucial role in the anti-microbial and anti-tumour activity of these cells. The data which were obtained show that P40ext stimulates the production of nitrite from RAW 264.7 cells, demonstrating that P40ext activates macrophages.

2. P40 is a carrier, with an adjuvant effect, for a peptide (G1ΔC)

2.1. Comparison of P40ext with other supports

5 The peptide which is used is G1ΔC, which is a peptide obtained from protein G of RSV: (G174-187 ΔC) Trudel et al., 1991, J. Virol. 185: 749-757.

Kinetics of the immune response to G1 ΔC

10 C57Bl/6 mice (5 per group) are immunized with different forms of G1 ΔC in accordance with an identical immunization protocol. The antibody responses induced by the different forms of G1 ΔC are compared at times of 7, 17, 28, 35 and 42 days after the start of the experiment.

15 The anti-G1 ΔC response is significantly greater and more rapid when the mice are immunized with P40/G1 ΔC than when they are immunized in the more conventional way with TT/G1 ΔC or KLH/G1 ΔC+FA. A single injection of P40/G1 ΔC results, in 7 days, in an anti-G1 ΔC antibody titre of 1000. With TT/G1 ΔC + FA, this titre is obtained in 28 days. The maximum response (titre = 1/380000),
20 obtained after three injections, in 28 days, is approximately 30 times greater than that obtained with KLH/G1 ΔC + FA, and 70 times greater than that obtained with TT/G1 ΔC. The anti-G1 antibody titre persists, without diminishing, up to day 42.

25 Conclusion

Chemically coupling the G1 ΔC peptide to the P40 protein rendered it possible to induce an anti-G1 ΔC response which was as great as that obtained with the KLH/G1 ΔC + FA or TT/G1 ΔC reference models.

30 The results obtained demonstrate that P40ext is a carrier molecule for G1ΔC which has an adjuvant effect: P40ext is superior to tetanus toxin and as good as the combination KLH + Freund's adjuvant.

2.1. Isotype distribution of the anti-GlΔC peptide antibodies

The isotypes of the sera obtained during the above-described experiments were determined by ELISA.

5 Table 4 gives the means of the A450 values of 5 individual sera which were tested at a dilution of 1/250.

Table 4: Isotype distribution of the anti-GlΔC peptide antibodies

	IgG1	IgG2a	IgG2b	IgG3
10 A450 (dil. 1/250)	2.892	1.212	2.970	0.209

It has been shown that the secretion of antibody isotype is regulated by subsets of antigen-specific Th cells, which can be divided into two subsets, Th1 and Th2. The Th1 clones produce IL-2 and IFN gamma and lymphotoxins, while the Th2 clones produce IL-4 and IL-5. The Th1 and Th2 clones specifically induce the secretion of IgG2a + IgG3 and IgG1 + IgG2b + IgE, respectively, by antigen-specific B cells. The data presented in Table 4 show that IgG1 and IgG2b are the two main isotypes of anti-GlΔC antibodies, with IgG2a also being represented. It may be concluded that, in C57B1/6 mice, P40-GlΔC provokes a Th2 response which is greater than the Th1 response.

25 2.2 Dose-effect study

Different concentrations of P40ext-GlΔC were injected subcutaneously, on days 0, 10 and 21, into BALB/c mice (5 per group). One week after the last immunization, blood samples are withdrawn and the anti-GlΔC peptide antibody response is measured by ELISA in the individual sera. The mean of the titres of 5 samples

is calculated.

Figure 5 shows the dose-effect relationship for P40ext-G1ΔC. An anti-G1ΔC peptide antibody response is obtained with 1 μg of P40ext-G1ΔC. The highest antibody
5 titres are observed with 10 to 50 μg of P40ext-G1ΔC.

2.4 Determination of the optimum immunization protocol

P40ext-G1ΔC (equivalent to 10 μg of G1ΔC) was injected subcutaneously, on the days indicated in Figure 6, into BALB/c mice (5 per group). The anti-G1ΔC
10 peptide antibody response is measured by ELISA on the individual sera. 4 immunization protocols were tested: one injection, two injections on days 0 and 14, or on days 0 and 21, and three injections on days 0, 21 and 40. The greatest anti-G1ΔC peptide antibody response is
15 obtained with three injections.

3. P40ext is an efficient adjuvant for a protein antigen (BBG2ΔC)

BBG2ΔC conjugated chemically with P40ext (equivalent to 10 μg of G2ΔC) was injected subcutaneously, on
20 days 0 and 21, into BALB/c mice (5 per group). Ten days later, the anti-G2ΔC antibody response is measured by ELISA in the individual sera. The means of the titres of 5 samples are given in Table 5. The negative control did not contain anti-G2ΔC antibody.

25 Table 5: Adjuvant effect of P40ext on a protein antigen

	Anti-G2ΔC antibody titre
BBG2ΔC	160
BBG2ΔC + Freund's adjuvant	2051200
extP40-BBG2ΔC	29800

BBG2ΔC is weakly immunogenic. Using Freund's adjuvant increases the titre of anti-G2ΔC antibody. When BBG2ΔC is conjugated chemically to P40ext, the anti-G2ΔC antibody response is increased approximately 200-fold. Therefore, P40ext is a good adjuvant for a protein antigen.

4. Adjuvant activity of P40 fragments

BALB/c mice (5 per group) were injected subcutaneously on day 0, and stimulated on day 21, with the following recombinant proteins: fusion protein BBP40G2ΔC, the fusion protein containing P40 fragment No. 8 (BB8G2ΔC), the fusion protein containing P40 fragment No. 16 (BB16G2ΔC) and the fusion protein containing P40 fragment No. 18 (BB18G2ΔC) (equivalent to 10 μg of G2ΔC).

On day 31, the anti-G2ΔC, anti-P40 and anti-BB antibody responses are measured by ELISA in the individual sera. The means of the titres of 5 individual sera are calculated. The negative controls did not contain anti-G2ΔC antibody.

Table 6: Adjuvant effect of the recombinant P40 fragments

	TITRE OF ANTI-G2ΔC ANTIBODY	TITRE OF ANTI-BB ANTIBODY	TITRE OF ANTI-P40 ANTIBODY
BBP40G2ΔC	14 800—	266 240	450 506
BB8G2ΔC	7 400	430 080	56 640
BB16G2ΔC	1 800	84 480	880
BB18G2ΔC	1 360	184 320	240

This experiment shows that the P40 fragments retain the properties of the complete protein. This is particularly striking when the anti-BB antibody response is considered.

The anti-P40 antibody response is considerably reduced when fragments of P40 are used.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT

5 (A) NAME: Pierre Fabre Medicaments
(B) STREET: 45, Place Abel Gance
(C) TOWN: Boulogne
(E) COUNTRY: France
(F) POSTAL CODE: 92654

(ii) TITLE OF INVENTION: Protein P40

10 (iii) NUMBER OF SEQUENCES: 8

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
15 (D) SOFTWARE: PatentIn Release #1.0,
Version #1.25 (OEB)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 1008 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

25 (A) NAME/KEY: CDS
(B) LOCATION: 1..1008

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GCT CCG AAA GAT AAC ACC TGG TAT GCA GGT GGT AAA CTG GGT TGG TCC
Ala Pro Lys Asp Asn Thr Trp Tyr Ala Gly Gly Lys Leu Gly Trp Ser
1 5 10 15

CAG TAT CAC GAC ACC GGT TTC TAC GGT AAC GGT TTC CAG AAC AAC AAC Gln Tyr His Asp Thr Gly Phe Tyr Gly Asn Gly Phe Gln Asn Asn Asn 20 25 30	96
GGT CCG ACC CGT AAC GAT CAG CTT GGT GCT GGT GCG TTC GGT GGT TAC Gly Pro Thr Arg Asn Asp Gln Leu Gly Ala Gly Ala Phe Gly Gly Tyr 35 40 45	144
CAG GTT AAC CCG TAC CTC GGT TTC GAA ATG GGT TAT GAC TGG CTG GGC Gln Val Asn Pro Tyr Leu Gly Phe Glu Met Gly Tyr Asp Trp Leu Gly 50 55 60	192
CGT ATG GCA TAT AAA GGC AGC GTT GAC AAC GGT GCT TTC AAA GCT CAG Arg Met Ala Tyr Lys Gly Ser Val Asp Asn Gly Ala Phe Lys Ala Gln 65 70 75 80	240
GGC GTT CAG CTG ACC GCT AAA CTG GGT TAC CCG ATC ACT GAC GAT CTG Gly Val Gln Leu Thr Ala Lys Leu Gly Tyr Pro Ile Thr Asp Asp Leu 85 90 95	288
GAC ATC TAC ACC CGT CTG GGC GGC ATG GTT TGG CGC GCT GAC TCC AAA Asp Ile Tyr Thr Arg Leu Gly Gly Met Val Trp Arg Ala Asp Ser Lys 100 105 110	336
GGC AAC TAC GCT TCT ACC GGC GTT TCC CGT AGC GAA CAC GAC ACT GGC Gly Asn Tyr Ala Ser Thr Gly Val Ser Arg Ser Glu His Asp Thr Gly 115 120 125	384
GTT TCC CCA GTA TTT GCT GGC GGC GTA GAG TGG GCT GTT ACT CGT GAC Val Ser Pro Val Phe Ala Gly Gly Val Glu Trp Ala Val Thr Arg Asp 130 135 140	432
ATC GCT ACC CGT CTG GAA TAC CAG TGG GTT AAC AAC ATC GGC GAC GCG Ile Ala Thr Arg Leu Glu Tyr Gln Trp Val Asn Asn Ile Gly Asp Ala 145 150 155 160	480
GGC ACT GTG GGT ACC CGT CCT GAT AAC GGC ATG CTG AGC CTG GGC GTT Gly Thr Val Gly Thr Arg Pro Asp Asn Gly Met Leu Ser Leu Gly Val 165 170 175	528
TCC TAC CGC TTC GGT CAG GAA GAT GCT GCA CCG GTT GTT GCT CCG GCT Ser Tyr Arg Phe Gly Gln Glu Asp Ala Ala Pro Val Val Ala Pro Ala 180 185 190	576
CCG GCT CCG GCT CCG GAA GTG GCT ACC AAG CAC TTC ACC CTG AAG TCT Pro Ala Pro Ala Pro Glu Val Ala Thr Lys His Phe Thr Leu Lys Ser 195 200 205	624
GAC GTT CTG TTC AAC TTC AAC AAA GCT ACC CTG AAA CCG GAA GGT CAG Asp Val Leu Phe Asn Phe Asn Lys Ala Thr Leu Lys Pro Glu Gly Gln 210 215 220	672
CAG GCT CTG GAT CAG CTG TAC ACT CAG CTG AGC AAC ATG GAT CCG AAA Gln Ala Leu Asp Gln Leu Tyr Thr Gln Leu Ser Asn Met Asp Pro Lys 225 230 235 240	720
GAC GGT TCC GCT GTT GTT CTG GGC TAC ACC GAC CGC ATC GGT TCC GAA Asp Gly Ser Ala Val Val Leu Gly Tyr Thr Asp Arg Ile Gly Ser Glu 245 250 255	768
GCT TAC AAC CAG CAG CTG TCT GAG AAA CGT GCT CAG TCC GTT GTT GAC Ala Tyr Asn Gln Gln Leu Ser Glu Lys Arg Ala Gln Ser Val Val Asp 260 265 270	816

TAC CTG GTT GCT AAA GGC ATC CCG GCT GGC AAA ATC TCC GCT CGC GGC	864
Tyr Leu Val Ala Lys Gly Ile Pro Ala Gly Lys Ile Ser Ala Arg Gly	
275 280 285	
ATG GGT GAA TCC AAC CCG GTT ACT GGC AAC ACC TGT GAC AAC GTG AAA	912
Met Gly Glu Ser Asn Pro Val Thr Gly Asn Thr Cys Asp Asn Val Lys	
290 295 300	
GCT CGC GCT GCC CTG ATC GAT TGC CTG GCT CCG GAT CGT CGT GTA GAG	960
Ala Arg Ala Ala Leu Ile Asp Cys Leu Ala Pro Asp Arg Arg Val Glu	
305 310 315 320	
ATC GAA GTT AAA GGC TAC AAA GAA GTT GTA ACT CAG CCG GCG GGT TA	1008
Ile Glu Val Lys Gly Tyr Lys Glu Val Val Thr Gln Pro Ala Gly	
325 330 335	

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 335 amino acids

(B) TYPE: amino acid

5

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Ala Pro Lys Asp Asn Thr Trp Tyr Ala Gly Gly Lys Leu Gly Trp Ser	
1 5 10 15	
Gln Tyr His Asp Thr Gly Phe Tyr Gly Asn Gly Phe Gln Asn Asn Asn	
20 25 30	
Gly Pro Thr Arg Asn Asp Gln Leu Gly Ala Gly Ala Phe Gly Gly Tyr	
35 40 45	
Gln Val Asn Pro Tyr Leu Gly Phe Glu Met Gly Tyr Asp Trp Leu Gly	
50 55 60	
Arg Met Ala Tyr Lys Gly Ser Val Asp Asn Gly Ala Phe Lys Ala Gln	
65 70 75 80	
Gly Val Gln Leu Thr Ala Lys Leu Gly Tyr Pro Ile Thr Asp Asp Leu	
85 90 95	
Asp Ile Tyr Thr Arg Leu Gly Gly Met Val Trp Arg Ala Asp Ser Lys	
100 105 110	
Gly Asn Tyr Ala Ser Thr Gly Val Ser Arg Ser Glu His Asp Thr Gly	
115 120 125	

Val	Ser	Pro	Val	Phe	Ala	Gly	Gly	Val	Glu	Trp	Ala	Val	Thr	Arg	Asp
130						135					140				
Ile	Ala	Thr	Arg	Leu	Glu	Tyr	Gln	Trp	Val	Asn	Asn	Ile	Gly	Asp	Ala
145					150					155					160
Gly	Thr	Val	Gly	Thr	Arg	Pro	Asp	Asn	Gly	Met	Leu	Ser	Leu	Gly	Val
				165					170					175	
Ser	Tyr	Arg	Phe	Gly	Gln	Glu	Asp	Ala	Ala	Pro	Val	Val	Ala	Pro	Ala
			180					185					190		
Pro	Ala	Pro	Ala	Pro	Glu	Val	Ala	Thr	Lys	His	Phe	Thr	Leu	Lys	Ser
		195					200					205			
Asp	Val	Leu	Phe	Asn	Phe	Asn	Lys	Ala	Thr	Leu	Lys	Pro	Glu	Gly	Gln
	210					215					220				
Gln	Ala	Leu	Asp	Gln	Leu	Tyr	Thr	Gln	Leu	Ser	Asn	Met	Asp	Pro	Lys
225					230					235					240
Asp	Gly	Ser	Ala	Val	Val	Leu	Gly	Tyr	Thr	Asp	Arg	Ile	Gly	Ser	Glu
				245					250					255	
Ala	Tyr	Asn	Gln	Gln	Leu	Ser	Glu	Lys	Arg	Ala	Gln	Ser	Val	Val	Asp
			260					265					270		
Tyr	Leu	Val	Ala	Lys	Gly	Ile	Pro	Ala	Gly	Lys	Ile	Ser	Ala	Arg	Gly
	275						280					285			
Met	Gly	Glu	Ser	Asn	Pro	Val	Thr	Gly	Asn	Thr	Cys	Asp	Asn	Val	Lys
	290					295					300				
Ala	Arg	Ala	Ala	Leu	Ile	Asp	Cys	Leu	Ala	Pro	Asp	Arg	Arg	Val	Glu
305					310					315					320
Ile	Glu	Val	Lys	Gly	Tyr	Lys	Glu	Val	Val	Thr	Gln	Pro	Ala	Gly	
				325					330					335	

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..537

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GCT	CCG	AAA	GAT	AAC	ACC	TGG	TAT	GCA	GGT	GGT	AAA	CTG	GGT	TGG	TCC	48
Ala	Pro	Lys	Asp	Asn	Thr	Trp	Tyr	Ala	Gly	Gly	Lys	Leu	Gly	Trp	Ser	
1				5					10					15		
CAG	TAT	CAC	GAC	ACC	GGT	TTC	TAC	GGT	AAC	GGT	TTC	CAG	AAC	AAC	AAC	96
Gln	Tyr	His	Asp	Thr	Gly	Phe	Tyr	Gly	Asn	Gly	Phe	Gln	Asn	Asn	Asn	
			20					25					30			
GGT	CCG	ACC	CGT	AAC	GAT	CAG	CTT	GGT	GCT	GGT	GCG	TTC	GGT	GGT	TAC	144
Gly	Pro	Thr	Arg	Asn	Asp	Gln	Leu	Gly	Ala	Gly	Ala		Phe	Gly	Gly	Tyr
		35					40					45				
CAG	GTT	AAC	CCG	TAC	CTC	GGT	TTC	GAA	ATG	GGT	TAT	GAC	TGG	CTG	GGC	192
Gln	Val	Asn	Pro	Tyr	Leu	Gly	Phe	Glu	Met	Gly	Tyr	Asp	Trp	Leu	Gly	
	50					55					60					
CGT	ATG	GCA	TAT	AAA	GGC	AGC	GTT	GAC	AAC	GGT	GCT	TTC	AAA	GCT	CAG	240
Arg	Met	Ala	Tyr	Lys	Gly	Ser	Val	Asp	Asn	Gly	Ala	Phe	Lys	Ala	Gln	
65					70					75					80	
GGC	GTT	CAG	CTG	ACC	GCT	AAA	CTG	GGT	TAC	CCG	ATC	ACT	GAC	GAT	CTG	288
Gly	Val	Gln	Leu	Thr	Ala	Lys	Leu	Gly	Tyr	Pro	Ile	Thr	Asp	Asp	Leu	
				85					90					95		
GAC	ATC	TAC	ACC	CGT	CTG	GGC	GGC	ATG	GTT	TGG	CGC	GCT	GAC	TCC	AAA	336
Asp	Ile	Tyr	Thr	Arg	Leu	Gly	Gly	Met	Val	Trp	Arg	Ala	Asp	Ser	Lys	
			100					105					110			
GGC	AAC	TAC	GCT	TCT	ACC	GGC	GTT	TCC	CGT	AGC	GAA	CAC	GAC	ACT	GGC	384
Gly	Asn	Tyr	Ala	Ser	Thr	Gly	Val	Ser	Arg	Ser	Glu	His	Asp	Thr	Gly	
		115					120					125				
GTT	TCC	CCA	GTA	TTT	GCT	GGC	GGC	GTA	GAG	TGG	GCT	GTT	ACT	CGT	GAC	432
Val	Ser	Pro	Val	Phe	Ala	Gly	Gly	Val	Glu	Trp	Ala	Val	Thr	Arg	Asp	
	130					135					140					
ATC	GCT	ACC	CGT	CTG	GAA	TAC	CAG	TGG	GTT	AAC	AAC	ATC	GGC	GAC	GCG	480
Ile	Ala	Thr	Arg	Leu	Glu	Tyr	Gln	Trp	Val	Asn	Asn	Ile	Gly	Asp	Ala	
145					150					155					160	
GGC	ACT	GTG	GGT	ACC	CGT	CCT	GAT	AAC	GGC	ATG	CTG	AGC	CTG	GGC	GTT	528
Gly	Thr	Val	Gly	Thr	Arg	Pro	Asp	Asn	Gly	Met	Leu	Ser	Leu	Gly	Val	
				165					170					175		
TCC	TAC	CGC														537
Ser	Tyr	Arg														

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 amino acids

(B) TYPE: amino acid

5

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Ala Pro Lys Asp Asn Thr Trp Tyr Ala Gly Gly Lys Leu Gly Trp Ser
1 5 10 15
Gln Tyr His Asp Thr Gly Phe Tyr Gly Asn Gly Phe Gln Asn Asn Asn
20 25 30
Gly Pro Thr Arg Asn Asp Gln Leu Gly Ala Gly Ala Phe Gly Gly Tyr
35 40 45
Gln Val Asn Pro Tyr Leu Gly Phe Glu Met Gly Tyr Asp Trp Leu Gly
50 55 60
Arg Met Ala Tyr Lys Gly Ser Val Asp Asn Gly Ala Phe Lys Ala Gln
65 70 75 80
Gly Val Gln Leu Thr Ala Lys Leu Gly Tyr Pro Ile Thr Asp Asp Leu
85 90 95
Asp Ile Tyr Thr Arg Leu Gly Gly Met Val Trp Arg Ala Asp Ser Lys
100 105 110
Gly Asn Tyr Ala Ser Thr Gly Val Ser Arg Ser Glu His Asp Thr Gly
115 120 125
Val Ser Pro Val Phe Ala Gly Gly Val Glu Trp Ala Val Thr Arg Asp
130 135 140
Ile Ala Thr Arg Leu Glu Tyr Gln Trp Val Asn Asn Ile Gly Asp Ala
145 150 155 160
Gly Thr Val Gly Thr Arg Pro Asp Asn Gly Met Leu Ser Leu Gly Val
165 170 175
Ser Tyr Arg

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CGC	GCT	GAC	TCC	AAA	GGC	AAC	TAC	GCT	TCT	ACC	GGC	GTT	TCC	CGT	AGC	48
Arg	Ala	Asp	Ser	Lys	Gly	Asn	Tyr	Ala	Ser	Thr	Gly	Val	Ser	Arg	Ser	
1				5				10						15		
GAA	CAC	GAC	ACT	GGC	GTT	TCC	CCA	GTA	TTT	GCT	GGC	GGC	GTA	GAG	TGG	96
Glu	His	Asp	Thr	Gly	Val	Ser	Pro	Val	Phe	Ala	Gly	Gly	Val	Glu	Trp	
			20					25						30		
GCT	GTT	ACT	CGT	GAC	ATC	GCT	ACC	CGT	CTG	GAA	TAC	CAG	TGG	GTT	AAC	144
Ala	Val	Thr	Arg	Asp	Ile	Ala	Thr	Arg	Leu	Glu	Tyr	Gln	Trp	Val	Asn	
			35					40					45			
AAC	ATC	GGC	GAC	GCG	GGC	ACT	GTG	GGT	ACC	CGT	CCT	GAT	AAC	GGC	ATG	192
Asn	Ile	Gly	Asp	Ala	Gly	Thr	Val	Gly	Thr	Arg	Pro	Asp	Asn	Gly	Met	
		50					55				60					
CTG	AGC	CTG	GGC	GTT	TCC	TAC	CGC									216
Leu	Ser	Leu	Gly	Val	Ser	Tyr	Arg									
65						70										

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Arg	Ala	Asp	Ser	Lys	Gly	Asn	Tyr	Ala	Ser	Thr	Gly	Val	Ser	Arg	Ser
1				5				10						15	
Glu	His	Asp	Thr	Gly	Val	Ser	Pro	Val	Phe	Ala	Gly	Gly	Val	Glu	Trp
			20					25					30		
Ala	Val	Thr	Arg	Asp	Ile	Ala	Thr	Arg	Leu	Glu	Tyr	Gln	Trp	Val	Asn
			35					40					45		
Asn	Ile	Gly	Asp	Ala	Gly	Thr	Val	Gly	Thr	Arg	Pro	Asp	Asn	Gly	Met
		50					55				60				
Leu	Ser	Leu	Gly	Val	Ser	Tyr	Arg								
65						70									

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..159

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ACT GGC GTT TCC CCA GTA TTT GCT GGC GGC GTA GAG TGG GCT GTT ACT	48
Thr Gly Val Ser Pro Val Phe Ala Gly Gly Val Glu Trp Ala Val Thr	
1 5 10 15	
CGT GAC ATC GCT ACC CGT CTG GAA TAC CAG TGG GTT AAC AAC ATC GGC	96
Arg Asp Ile Ala Thr Arg Leu Glu Tyr Gln Trp Val Asn Asn Ile Gly	
20 25 30	
GAC GCG GGC ACT GTG GGT ACC CGT CCT GAT AAC GGC ATG CTG AGC CTG	144
Asp Ala Gly Thr Val Gly Thr Arg Pro Asp Asn Gly Met Leu Ser Leu	
35 40 45	
GGC GTT TCC TAC CGC	159
Gly Val Ser Tyr Arg	
50	

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 amino acids

(B) TYPE: amino acid

10

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Thr Gly Val Ser Pro Val Phe Ala Gly Gly Val Glu Trp Ala Val Thr	
1 5 10 15	
Arg Asp Ile Ala Thr Arg Leu Glu Tyr Gln Trp Val Asn Asn Ile Gly	
20 25 30	
Asp Ala Gly Thr Val Gly Thr Arg Pro Asp Asn Gly Met Leu Ser Leu	
35 40 45	
Gly Val Ser Tyr Arg	
50	